

FIGURE 1

FT sense insert (814 bp without vector sequences)

Xba I

TCTAGAACTAGTGGATCCCCGGGCTCCAGGAATTCAAGCACGAGGTTTGTCAAGATCAAAG

ATGTCTATAAATATAAGAGACCCTCTATAGTAAGCAGAGTTGGAGACGTTCTGAT
MetSerIleAsnIleArgAspProLeuIleValSerArgValValGlyAspValLeuAsp

CCGTTAATAGATCAATCACTCTAAAGGTTACTTATGGCCAAAGAGAGGTTGACTAATGGC
ProPheAsnArgSerIleThrLeuLysValThrTyrGlyGlnArgGluValThrAsnGly

TTGGATCTAAGCCTCTCAGGTTAAAACAAGCCAAGAGTTGAGATTGGTGGAGAAGAC
LeuAspLeuArgProSerGlnValGlnAsnLysProArgValGluIleGlyGlyGluAsp

CTCAGGAACCTCTATACTTTGGTTATGGTGGATCCAGATGTTCCAAGTCCTAGCAACCCCT
LeuArgAsnPheTyrThrLeuValMetValAspProAspValProSerProSerAsnPro

CACCTCCGAGAATATCTCCATTGGTTGGTGA
CTGATATCCTGCTACAACTGGAACAA
CC HisLeuArgGluTyrLeuHisTrpLeuValThrAspIleProAlaThrThrGlyThrThr

TTTGGCAATGAGATTGTGTACGAAAATCCAAGTCCCACTGCAGGAATTATCGTGTC
PheGlyAsnGluIleValCysTyrGluAsnProSerProThrAlaGlyIleHisArgVal

GTGTTTATATTGTTGACAGCTGGCAGGCAAACAGTGTATGCACCAGGGTGGCGCCAG
ValPheIleLeuPheArgGlnLeuGlyArgGlnThrValTyrAlaProGlyTrpArgGln

AACTTCAACACTCGCGAGTTGCTGAGATCTAACATCTGGCCTTCCCGTGGCCGCAGTT
AsnPheAsnThrArgGluPheAlaGluIleTyrAsnLeuGlyLeuProValAlaAlaVal

TTCTACAATTGTCAGAGGGAGGTGGCTGCGGAGGAAGAAGACTTAGATGGCTTCTTCC
PheTyrAsnCysGlnArgGluSerGlyCysGlyGlyArgArgLeu***

TTTATAACCAATTGATATTGCATACTCTGATGAGATTATGCATCTATAGTATTAAATT
TAATAACCATTATGATACGAGTAACGAACGGTGTGATGCCTATAGTAGTTCAATATA
TAAGTGTGTAATAAAATGAGAGGGGGAGGAAAATGAGAGTGTTTACTTATATAGTGTG
TGATGCGATAATTATATTACATGAAATGAAGTGTATATTATAAAAAAAAAAAAAA

Xho I
AAAAAAAACCTCGAG

FT antisense sense insert (814 bp without vector sequences)

CTCGAGTTTTTTTTTTTTTATAAAATATAACACTCATTCATGAGATTAAATA
TAATTATCGCATCACACACTATATAAGTAAAACACTCTCATTTCCTCCCCCTCATT
TTATTACACACTTATATATTGAACACTATAGGCATCATACCAGTTCGTTACTCGTATCA
TAAAATGGTTATTAAATTAAAATACTATAGATGCATAAAATCTCATCAGAGTATGCAATAT
CAATTGGTTATAAAGGAAGAGCCATCTAAAGTCTTCTCCGCCAGCCACTCTCCCTC
TGACAATTGTAGAAAATCGGGCCACGGGAAGGCCAGATTGTAGATCTCAGCAAATCTG
CGAGTGGTGAAGTTCTGGGCCACCCGGTGCATACACTGTTGCCCTGCCAAGCTGTCGA
AACAAATATAAACACGACACGGATGAATTCTGCAGTGGACTTGGATTTCGTAACACACA
ATCTCATTGCCAAGGGTGGTCCAGTTGAGCAGGGATATCAGTCACCAACCAATGGAGA
TATTCTGGAGGTGAGGGTGTCTAGGACTTGGAACATCTGGATCCACCAACCAAGTA
TAGAAGTTCTGAGGTCTCTCCACCAATCTCAACTCTGGCTTGTGAAACCTGAGAA
GGCCTAGATCCAAGCCATTAGTCACCTCTCTTGGCCATAAGTAACCTTAGAGTGATT
GATCTATTAAACGGATCAAGAACGTCTCCAACAACACTCTGTTACTATAAGAGGGTCTCT
ATATTTATAGACATCTTGATCTGAAACAAACCTCGTGTGAATTCTGCAGCCCCGGGGG

Xba I
ATCCACTAGTTCTAGA

FIGURE 2

FIGURE 3A

1	M-----DPLIV.RVVGDVLD.F.....L.V.YG...VTN-G..L.PSQV.NKPR-VEI.G.DLR	At	FT
1	M.....PLI.GRVGDVLD.F.PT.....V.Y..K.V.N-G.EL.PS.V..KPR-VEI.G.DLR	At	TFL1
1	MAA----DPLI.GRVGDVLD.F.PT.....V.Y..K.V.N-G.EL.PS.V..KPR-VEI.G.DLR	At	E12A11
1	MAA.....PL.....V.....P...L.V.YG...V...G..L.P.QV.N.P.....G.D..	Rn	HCNP
63	YTLVM.DPD.PSPS.P.LRE.IHHLV.DIP.TT...FG.EIV.YE.P.P...GIHR.VF.LFRQ	At	FT
66	YTLVM.DPD.P.PSDP.L.E.LHW.V..IPGTTD..FGKE.V.YE.PRP...GIHR.VFVLFRQ	At	TFL1
61	.LYTLVMTDPDAPS.P.P.REW.HW.VVDIPG.T..S.GKEI..Y..PRPP...GIHRY..VLFRQ	At	E12A11
62	.LYTLV.TDPDAPS..DP..REW.H.LVV..G.-D.S.G...Y...PP...G.HRYV.....Q		
128	..R-----G..R.NFNTR.FA..Y.LGLPVAAVF.N.QRE...RR-----.	At	FT
131	..QR-----G..SR..FNTR.FA..YDLGLPVAAVF.NAQRE..--A.RR-----R.	At	TFL1
126	...----.L.....G..SR..NF..TR.FA...DLGLPVA.VF.NAQRE..--A.RR-----R.	At	E12A11
128	Q.....L...G..R...F...F..Y.LG.PVA...F.AQRE.....	Rn	HCNP

FIGURE 3C

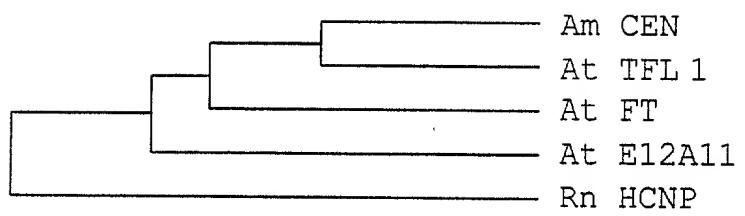


FIGURE 3B